Amendments to the Claims

Please cancel claims 1-10 without prejudice. Please add new claims 11-27 as shown below in the List of Claims.

List of Claims

1-10. Cancelled.

11. (New) A process for producing an L-amino acid comprising:

a) culturing a modified enterobacterium of the genus *Escherichia* in a medium for a time and under conditions suitable for producing said L-amino acid; and

b) recovering or isolating said L-amino acid;

wherein the *yjgF* open reading frame of said modified enterobacterium has been inactivated by one or more methods of mutagenesis selected from the group consisting of: deletion of all or part of the *yjgF* open reading frame; insertional mutagenesis due to homologous recombination; and transitional or transversional mutagenesis with incorporation of a non-sense mutation in the *yjgF* open reading frame;

wherein said *yjgF* open reading frame is obtainable from *Escherichia* by PCR amplification using primer yjgF-1 (SEQ ID NO: 3) and primer yjgF-4 (SEQ ID NO:6).

12. (New) The process of claim 11, wherein said *yjgF* open reading frame encodes the polypeptide of SEQ ID NO:2.

13. (New) The process of claim 11, wherein said *yjgF* open reading frame has the nucleotide sequence of SEQ ID NO:1.

14. (New) The process of claim 11, wherein said L-amino-acid is selected from the group consisting of: L-asparagine; L-serine; L-glutamate; L-glycine; L-alanine; L-cysteine; L-valine; L-methionine; L-isoleucine; L-leucine; L-tyrosine; L-phenylalanine; L-histidine; L-lysine; L-tryptophan; and L-arginine.

15. (New): The process of claim 11, wherein said L-amino acid is L-threonine.

16. (New) The process of claim 11, wherein constituents of the fermentation broth and/or the biomass in its entirety or portions thereof remain in the isolated L-amino acid.

17. (New) The process of claim 11, wherein said modified enterobacterium of the genus *Escherichia* further comprises at least one overexpressed gene product, achieved by increasing the copy number of the gene or placing the gene under a strong promoter, compared to the unmodified *Escherichia*, wherein the gene product is encoded by a gene selected from the group consisting of:

a) a *thrA* gene coding for aspartate kinase / homoserine dehydrogenase I;
b) a *thrB* gene coding for homoserine kinase;
c) a *thrC* gene coding for threonine synthase;
d) the *Corynebacterium glutamicum pyc* gene coding for pyruvate carboxylase;
e) a *pps* gene coding for phosphoenol pyruvate synthase;
f) a *ppc* gene coding for phosphoenol pyruvate carboxylase;
g) a *pntA* and a *pntB* genes coding for the subunits of pyridine transhydrogenase;
h) the *Escherichia coli rhtB* gene coding for a protein imparting homoserine resistance;
i) a *mqo* gene coding for malate:quinone oxidoreductase;
j) the *Escherichia coli rhtC* gene coding for a protein imparting threonine resistance;
k) the *Corynebacterium glutamicum thrE* gene coding for a threonine export carrier protein;
l) a gdhA gene encoding glutamate dehydrogenase;
m) a hns gene encoding the DNA-binding protein HLP-II;
n) a pgm gene encoding phosphoglucomutase;
o) a fba gene encoding fructose biphosphate aldolase;
p) a ptsH gene encoding the phosphohistidine protein hexose phosphotransferase;
q) a ptsI gene encoding enzyme I of the phosphotransferase system;
r) a crr gene encoding the glucose-specific IIA component;

s) a ptsG gene encoding the glucose-specific IIBC component;

t) a lrp gene encoding the regulator of the leucine regulon;

u) a csrA gene encoding the global regulator Csr;

v) a fadR gene encoding the regulator of the fad regulon;

w) a iclR gene encoding the regulator of central intermediate metabolism;

x) a mopB gene encoding the 10 Kd chaperone;

y) a ahpC gene encoding the small subunit of alkyl hydroperoxide reductase;

z) a ahpF gene encoding the large subunit of alkyl hydroperoxide reductase;

aa) a cysK gene encoding cysteine synthase A;

bb) a cysB gene encoding the regulator of the cys regulon;

cc) a cysJ gene encoding the flavoprotein of NADPH sulfite reductase;

dd) a cysI gene encoding the haemoprotein of NADPH sulfite reductase;

ee) a cysH gene encoding adenylyl sulfate reductase;

ff) a phoB gene encoding the positive regulator PhoB of the pho regulon;

gg) a phoR gene encoding the sensor protein of the pho regulon;

hh) a phoE gene encoding protein E of the outer cell membrane;

ii) a pykF gene which codes for fructose-stimulated pyruvate kinase I;

jj) a pfkB gene encoding 6-phosphofructokinase II;

kk) a malE gene encoding the periplasmic binding protein of maltose transport;

ll) a sodA gene encoding superoxide dismutase;

mm) a rseA gene encoding a protein with anti-sigmaE activity;

nn) a rseC gene encoding a global regulator of the sigmaE factor;

oo) a sucA gene encoding the decarboxylase subunit of 2-ketoglutarate dehydrogenase;

pp) a sucB gene coding for the dihydrolipoyltranssuccinase E2 subunit of 2 ketoglutarate dehydrogenase;

qq) a sucC gene encoding the beta-subunit of succinyl-CoA synthetase;

rr) a sucD gene encoding the alpha-subunit of succinyl-CoA synthetase;

ss) a adk gene encoding adenylate kinase;

tt) a hdeA gene coding for a periplasmic protein with a chaperonin-like function;

uu) a hdeB gene which codes for a periplasmic protein with a chaperonin-like function;

vv) a icd gene coding for isocitrate dehydrogenase;

ww) a mglB gene coding for the periplasmic galactose-binding transport protein;

xx) a lpd gene coding for dihydrolipoamide dehydrogenase;

yy) a aceE gene coding for the E1 component of the pyruvate dehydrogenase complex;

zz) a aceF gene coding for the E2 component of the pyruvate dehydrogenase complex;

aaa) a pepB gene coding for aminopeptidase B;

bbb) a aldH gene coding for aldehyde dehydrogenase;

ccc) a bfr gene coding for the iron storage homoprotein;

ddd) a udp gene which codes for uridine phosphorylase; and

eee) a rseB gene which codes for the regulator of sigmaE factor activity.

18. (New) The process of claim 11, wherein said modified enterobacterium of the genus *Escherichia* further comprises at least one gene which is inactivated by one or more methods of mutagenesis selected from the group consisting of deletion of all or part of the gene, insertional mutagenesis due to homologous recombination, and transition or transversion mutagenesis with incorporation of a non-sense mutation in the gene, compared to the unmodified *Escherichia*, wherein the at least one gene is selected from the group consisting of:

a) a *tdh* gene coding for threonine dehydrogenase;

b) a *mdh* gene coding for malate dehydrogenase;

c) the open reading frame (orf) *yjfA* of *E. coli*, when said modified *Escherichia* is *Escherichia coli*;

d) the open reading frame (orf) *ytfP* of *E. coli*, when said modified *Escherichia* is *Escherichia coli*;

e) a *pckA* gene coding for phosphoenol pyruvate carboxykinase;

f) a *poxB* gene coding for pyruvate oxidase;

g) an *aceA* gene coding for isocitrate lyase;

h) a *dgsA* gene coding for the regulator DgsA of the phosphotransferase system;

i) the *Escherichia coli fruR* gene coding for a fructose repressor;

j) a *rpoS* gene which codes for the sigma^{38} factor;

k) an *aspA* gene encoding aspartate ammonium lyase; and

l) an *aceB* gene encoding malate synthase A.

19. (New) The process of claim 11, wherein said *Escherichia* is *Escherichia coli.*

20. (New) The process of claim 11, wherein the expression of the *yjgF* open reading frame has been eliminated by the deletion of part of the *yjgF* open reading frame.

21. (New) The process of claim 11, wherein the expression of the *yjgF* open reading frame has been eliminated by the deletion of all of the *yjgF* open reading frame.

22. (New) The process of claim 11, wherein said L-amino acid is recovered from the modified *Escherichia.*

23. (New) The process of claim 11, wherein said L-amino acid is recovered from said medium.

24. (New) The process of claim 11, wherein culturing is continued until a maximum amount of the L-amino acid has been formed.

25. (New) The process of claim 11, wherein culturing is performed using a batch process.

26. (New) The process of claim 11, wherein culturing is performed using a fed batch process.

27. (New) The process of claim 11, wherein culturing is performed using a repeated fed batch process.